SEQUENCE LISTING

<110> Bowden, Donald W.
Dawson, Paul A.
Fossey, Sallyanne C.

<120> GLUT10: A Novel Glucose Transporter in the Type 2 Diabetes Linked Region of Chromosome 20Q12-13.1

<130> 9151-11

<140> US 09/652,292
<141> 2000-08-31

<160> 43

<170> PatentIn version 3.2

<210> 1
<211> 4395
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (250)..(1875)

<400> 1
gagggggtcc ttgccaggcc tggggcggcc gggggcggtc ctgggctccc ctccgtcccg 60

cctccaggcc tcggggcctg gctggccgac gtggcgttgg cggcgctgcg cgcgggaggg 120

cagggcagga gggacagagg cgggggcggg ccggaaagtt tgtccggcgg cagcggcgtt 180

ggggactccg gcgggggatg cgcgcccggc ccctcagcgc ccccagcacg ccgccgagtc 240

ccgctcgcc atg ggc cac tcc cca cct gtc ctg cct ttg tgt gcc tct gtg 291
Met Gly His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val
1 5 10

tct ttg ctg ggt ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca 339
Ser Leu Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser
15 20 25 30

ggt gcc ctg ctg cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag 387
Gly Ala Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu
35 40 45

cag gag ttc ctg gtg ggc agc ctg ctc ctg ggg gct ctc ctc gcc tcc 435
Gln Glu Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser
50 55 60

ctg gtt ggt ggc ttc ctc att gac tgc tat ggc agg aag caa gcc atc 483
Leu Val Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile
65 70 75

ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg 531
Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu
80 85 90

```
gct ggt tcc ctg gcc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc      579
Ala Gly Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe
95                  100                 105                 110

gcc att tcc ctc tcc tcc atg gct tgc tgt atc tac gtg tca gag ctg      627
Ala Ile Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu
                115                 120                 125

gtg ggg cca cgg cag cgg gga gtg ctg gtg tcc ctc tat gag gca ggc      675
Val Gly Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly
            130                 135                 140

atc acc gtg ggc atc ctg ctc tcc tat gcc ctc aac tat gca ctg gct      723
Ile Thr Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala
        145                 150                 155

ggt acc ccc tgg gga tgg agg cac atg ttc ggc tgg gcc act gca cct      771
Gly Thr Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro
    160                 165                 170

gct gtc ctg caa tcc ctc agc ctc ctc ttc ctc cct gct ggt aca gat      819
Ala Val Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp
175                 180                 185                 190

gag act gca aca cac aag gac ctc atc cca ctc cag gga ggt gag gcc      867
Glu Thr Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala
                195                 200                 205

ccc aag ctg ggc ccg ggg agg cca cgg tac tcc ttt ctg gac ctc ttc      915
Pro Lys Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe
            210                 215                 220

agg gca cgc gat aac atg cga ggc cgg acc aca gtg ggc ctg ggg ctg      963
Arg Ala Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu
        225                 230                 235

gtg ctc ttc cag caa cta aca ggg cag ccc aac gtg ctg tgc tat gcc     1011
Val Leu Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala
    240                 245                 250

tcc acc atc ttc agc tcc gtt ggt ttc cat ggg gga tcc tca gcc gtg     1059
Ser Thr Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val
255                 260                 265                 270

ctg gcc tct gtg ggg ctt ggc gca gtg aag gtg gca gct acc ctg acc     1107
Leu Ala Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr
                275                 280                 285

gcc atg ggg ctg gtg gac cgt gca ggc cgc agg gct ctg ttg cta gct     1155
Ala Met Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala
            290                 295                 300

ggc tgt gcc ctc atg gcc ctg tcc gtc agt ggc ata ggc ctc gtc agc     1203
Gly Cys Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser
        305                 310                 315

ttt gcc gtg ccc atg gac tca ggc cca agc tgt ctg gct gtg ccc aat     1251
Phe Ala Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn
    320                 325                 330

gcc acc ggg cag aca ggc ctc cct gga gac tct ggc ctg ctg cag gac     1299
```

```
Ala Thr Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp
335                 340                 345                 350

tcc tct cta cct ccc att cca agg acc aat gag gac caa agg gag cca     1347
Ser Ser Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro
                355                 360                 365

atc ttg tcc act gct aag aaa acc aag ccc cat ccc aga tct gga gac     1395
Ile Leu Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp
            370                 375                 380

ccc tca gcc cct cct cgg ctg gcc ctg agc tct gcc ctc cct ggg ccc     1443
Pro Ser Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro
        385                 390                 395

cct ctg ccc gct cgg ggg cat gca ctg ctg cgc tgg acc gca ctg ctg     1491
Pro Leu Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu
    400                 405                 410

tgc ctg atg gtc ttt gtc agt gcc ttc tcc ttt ggg ttt ggg cca gtg     1539
Cys Leu Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val
415                 420                 425                 430

acc tgg ctt gtc ctc agc gag atc tac cct gtg gag ata cga gga aga     1587
Thr Trp Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg
                435                 440                 445

gcc ttc gcc ttc tgc aac agc ttc aac tgg gcg gcc aac ctc ttc atc     1635
Ala Phe Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile
            450                 455                 460

agc ctc tcc ttc ctc gat ctc att ggc acc atc ggc ttg tcc tgg acc     1683
Ser Leu Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr
        465                 470                 475

ttc ctg ctc tac gga ctg acc gct gtc ctc ggc ctg ggc ttc atc tat     1731
Phe Leu Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr
    480                 485                 490

tta ttt gtt cct gaa aca aaa ggc cag tcg ttg gca gag ata gac cag     1779
Leu Phe Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln
495                 500                 505                 510

cag ttc cag aag aga cgg ttc acc ctg agc ttt ggc cac agg cag aac     1827
Gln Phe Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn
                515                 520                 525

tcc act ggc atc ccg tac agc cgc atc gag atc tct gcg gcc tcc tga     1875
Ser Thr Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser
            530                 535                 540

ggaatccgtc tgcctggaat tctggaactg tggctttggc agaccatctc cagcatcctg   1935

cttcctaggc cccagagcac aagttccagc tggtcttttg ggagtggccc ctgccccaa    1995

aggtggtttg cttttgctgg ggtaaaaagg atgaaagttt gagaatgccc aattcttcat   2055

tttgggtttc aggccctgaa ggttcttgag gatctagttt catgcctcgg tttccccatt   2115

gacttggaca tttttgcagt ttttataaga agaatattct atgaagtctt tgttgcccca   2175
```

tggatttttt tcaaagaatc tcaggggtac caatccgggc aggaggtttt tcccgatatc 2235

acccctaaat ccaaatgagg atatcatctt ttctaatctc ttttttcaac tggctgggac 2295

attttcggaa gggggaagtc tctttttta ctcttatcat tttttttttt tgaggtggag 2355

tctcattctg ttgcccaggc tggcctgatc ttggctcact gcaacctcca cttcctgggt 2415

tcaagcgatt ctcctgcctc agcctcctaa gtagctggga ttacaggcgc gtgccaccac 2475

acccagctaa tttatttta gcagagatgg ggtttcactg tgttggccag gctggtcgtg 2535

aactcctgag ctcaagtgat ccacccacct cagcctccca gagtgctagg attacaggcc 2595

ttttgactct tttatctgag ttttattgac ccctctaatt ctcttaccca gaatatttat 2655

ccttcaccag caactctgac tctttgacgg gaggcctcag ttctagtcct tggtctgctg 2715

gtgtcattgc tgtaggaatg accacgggcc tcagtttccc catttgtata atgggaagcc 2775

tgtaccaggt cattcttaag atttctcctg actccagtga gctggaattc taaatgctgg 2835

tctaggagct gtctccagga tggtgcagga tggctttgcg gaaaggagat gggtttggag 2895

gccaacaaac ctgcttgtca atattgcctt tgcctcttgg cagcccttga acttgagtaa 2955

ataacaactc cctgaacctc agtttcctca tctgcagaat ggggataatt atgtcccagg 3015

ggtatattta gaccctgttt cctttcagga gggtccccag ctggtccagg gcctgggaaa 3075

tttctactta tcctcattac ccaggtccct cctttggacc ctgtaaaggg tcagggtgaa 3135

tcagatgggg gactgagcaa gtagctatga ctgcagatca tgtaaggaag ggactgacaa 3195

gaagctccca gatgctgggg agaatgaaga gctaaaatag atcctaggtg ctggatgctt 3255

tgtcatccat gcgtgcacat atgggtgctg gcagagcccc caaggactct ggcctctcga 3315

gttctcctat cttctccatt ctagatgctt cccttgtatc cagtgatgtg ctggagctgg 3375

ctttgccaag cttgtgagag ctggttgcta cattttcagg atttttacaa gttggtaaac 3435

acagccatta taaaaaatta aatgatttaa atttataatt aagtaaatta cattaaaaca 3495

aaaaaattat actcaaaatt cattacttaa ttttactacc tgttactatt atctgtgctt 3555

ttgaggctat ttctacatag taactcttat ggagacctag gggagacacc gcgcatctct 3615

tcctgattcc ccactcaatg acatcatgtt agtctttggt tgcttaactg gctgtgggga 3675

gtgtttttgt atcacaaaga ttagagagga ctacacatca gggcttgatt tattgtttgt 3735

tgattttcta gacttcagaa catgctggat aaaatgtcag taatgcaaat taaactttaa 3795

agtatgtctt gtttgtagcc aatacatggt gtatagcacc aaaaaatgga gggattattc 3855

ttccagtagt tgaacactgt catccgtttc agctgacagc tgctcaaatc atttaagaag 3915

gagttctgac attcattttc attgttttac ttttgtcttc ctcactagtg taaacaaaaa 3975

tttcaaccag cattcatgcc gaacctatac ccattcttca gtgcctagct gtacagttat 4035

cagggatttt tattcgtagt ctaattttgt caaatcatgg ccaaatcgca gtgatagttg 4095

actttggata caaggtttgg caaaaaaaaa aatattaaca aaatattctg taagaatcaa 4155

ttggctatat ggaatttagg ataaagaata tttacaataa agaatattta caataaagag 4215

tttattatta tttgtaagtt gtgtgcaaca aacataccct ttatctctgt aaaatttata 4275

cacacaaaaa ttaacaaaag attctgtaag aattaattgg ctatatggaa tttaggatag 4335

aatatttaca ataaagagta tttacaataa agagtttgtt attatttgta aaaaaaaaaa 4395

<210> 2
<211> 541
<212> PRT
<213> Homo sapiens

<400> 2

Met Gly His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val Ser Leu
1 5 10 15

Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser Gly Ala
20 25 30

Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu Gln Glu
35 40 45

Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser Leu Val
50 55 60

Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly
65 70 75 80

Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly
85 90 95

Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile
100 105 110

Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly
115 120 125

Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr
130 135 140

Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr
145 150 155 160

Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro Ala Val
165 170 175

Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp Glu Thr
180 185 190

Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys
195 200 205

Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala
210 215 220

Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu
225 230 235 240

Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr
245 250 255

Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala
260 265 270

Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met
275 280 285

Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys
290 295 300

Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala
305 310 315 320

Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr
325 330 335

Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser
340 345 350

Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu
355 360 365

Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser
370 375 380

Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu
385 390 395 400

Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu

405 410 415

Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp
420 425 430

Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe
435 440 445

Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu
450 455 460

Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu
465 470 475 480

Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe
485 490 495

Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe
500 505 510

Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr
515 520 525

Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser
530 535 540

<210> 3
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 3
ggcacctctt ccctgcaaag 20

<210> 4
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 4
ccctcccgcg cgcagcgccg 20

<210> 5
<211> 18

<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 5
cgtcccgcct ccaggcct 18

<210> 6
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 6
ccatggcgag cgggact 17

<210> 7
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 7
cgtcccgcct ccaggcct 18

<210> 8
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 8
ggcggtgtct acaccctgg 19

<210> 9
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 9
tgacagatgg agggaaggtt g 21

<210> 10
<211> 19
<212> DNA

<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 10
aggagcaggc tgcccacca 19

<210> 11
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 11
ctggcagtca tatcaggtgc 20

<210> 12
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 12
aatggcgaag ccaaccacag 20

<210> 13
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 13
ggagcaactt ggtgctgctg 20

<210> 14
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 14
agtggcccag ccgaacatgt 20

<210> 15
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 15
ctcaactatg cactggctgg 20

<210> 16
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 16
cggagctgaa gatggtggag 20

<210> 17
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 17
ctcttccagc aactaacagg g 21

<210> 18
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 18
agcttgggcc tgagtccatg 20

<210> 19
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 19
agtggcatag gcctcgtcag 20

<210> 20
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 20
agaagtctcc agagtcacct g 21

<210> 21
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 21
ggctgcatgt ttgacctgat g 21

<210> 22
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 22
gctttagagt agggagcttg g 21

<210> 23
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 23
tgacctagaa cctaccagtt g 21

<210> 24
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 24
tcctgaagct gtgtgcttgg 20

<210> 25
<211> 19
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 25
gggaacccca gtggaaggt 19

<210> 26
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 26
caggcagacg gattcctcag 20

<210> 27
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 27
aactccactg gcatcccgt 19

<210> 28
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 28
catgaaacta gatcctcaag 20

<210> 29
<211> 16
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 1 5' splice donor

<400> 29
tcgccatggg taagtc 16

<210> 30
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 2 3' splice acceptor

<400> 30
tttttaggcc actcc 15

<210> 31
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 2 5' splice acceptor

<400> 31
gggccaggta agtg 14

<210> 32
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 3 3' splice acceptor

<400> 32
accctagtga cctgg 15

<210> 33
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 3 5' splice donor

<400> 33
ctcattggtg agtc 14

<210> 34
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 4 3' splice acceptor

<400> 34
tttccaggca ccatc 15

<210> 35
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 4 5' splice donor

<400> 35
aagagacggt aggaa 15

<210> 36
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Exon 5 3' splice acceptor

<400> 36
ctgacaggtt cacc 14

<210> 37
<211> 26
<212> DNA
<213> Homo sapiens

<220>
<221> 3'UTR
<222> (1)..(26)

<220>
<221> polyA_site
<222> (26)..(26)

<400> 37
aataaagagt ttgttattaa tttgta 26

<210> 38
<211> 492
<212> PRT
<213> Homo sapiens

<400> 38

Met Glu Pro Ser Ser Lys Lys Leu Thr Gly Arg Leu Met Leu Ala Val
1 5 10 15

Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val
20 25 30

Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp
35 40 45

Val His Arg Tyr Gly Glu Ser Ile Leu Pro Thr Thr Leu Thr Thr Leu
50 55 60

Trp Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser
65 70 75 80

Phe Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met
85 90 95

Leu Met Met Asn Leu Leu Ala Phe Val Ser Ala Val Leu Met Gly Phe
100 105 110

Ser Lys Leu Gly Lys Ser Phe Glu Met Leu Ile Leu Gly Arg Phe Ile
115 120 125

Ile Gly Val Tyr Cys Gly Leu Thr Thr Gly Phe Val Pro Met Tyr Val
130 135 140

Gly Glu Val Ser Pro Thr Ala Phe Arg Gly Ala Leu Gly Thr Leu His
145 150 155 160

Gln Leu Gly Ile Val Val Gly Ile Leu Ile Ala Gln Val Phe Gly Leu
165 170 175

Asp Ser Ile Met Gly Asn Lys Asp Leu Trp Pro Leu Leu Leu Ser Ile
180 185 190

Ile Phe Ile Pro Ala Leu Leu Gln Cys Ile Val Leu Pro Phe Cys Pro
195 200 205

Glu Ser Pro Arg Phe Leu Leu Ile Asn Arg Asn Glu Glu Asn Arg Ala
210 215 220

Lys Ser Val Leu Lys Lys Leu Arg Gly Thr Ala Asp Val Thr His Asp
225 230 235 240

Leu Gln Glu Met Lys Glu Glu Ser Arg Gln Met Met Arg Glu Lys Lys
245 250 255

Val Thr Ile Leu Glu Leu Phe Arg Ser Pro Ala Tyr Arg Gln Pro Ile

260 265 270

Leu Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn
275 280 285

Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Lys Ala Gly Val Gln
290 295 300

Gln Pro Val Tyr Ala Thr Ile Gly Ser Gly Ile Val Asn Thr Ala Phe
305 310 315 320

Thr Val Val Ser Leu Phe Val Val Glu Arg Ala Gly Arg Arg Thr Leu
325 330 335

His Leu Ile Gly Leu Ala Gly Met Ala Gly Cys Ala Ile Leu Met Thr
340 345 350

Ile Ala Leu Ala Leu Leu Glu Gln Leu Pro Trp Met Ser Tyr Leu Ser
355 360 365

Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Val Gly Pro Gly
370 375 380

Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
385 390 395 400

Pro Ala Ala Ile Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
405 410 415

Ile Val Gly Met Cys Phe Gln Tyr Val Glu Gln Leu Cys Gly Pro Tyr
420 425 430

Val Phe Ile Ile Phe Thr Val Leu Leu Val Leu Phe Phe Ile Phe Thr
435 440 445

Tyr Phe Lys Val Pro Glu Thr Lys Gly Arg Thr Phe Asp Glu Ile Ala
450 455 460

Ser Gly Phe Arg Gln Gly Gly Ala Ser Gln Ser Asp Lys Thr Pro Glu
465 470 475 480

Glu Leu Phe His Pro Leu Gly Ala Asp Ser Gln Val
485 490

<210> 39
<211> 524

<212> PRT
<213> Homo sapiens

<400> 39

```
Met Thr Glu Asp Lys Val Thr Gly Thr Leu Val Phe Thr Val Ile Thr
1               5                  10                  15

Ala Val Leu Gly Ser Phe Gln Phe Gly Tyr Asp Ile Gly Val Ile Asn
            20                  25                  30

Ala Pro Gln Gln Val Ile Ile Ser His Tyr Arg His Val Leu Gly Val
        35                  40                  45

Pro Leu Asp Asp Arg Lys Ala Ile Asn Asn Tyr Val Ile Asn Ser Thr
    50                  55                  60

Asp Glu Leu Pro Thr Ile Ser Tyr Ser Met Asn Pro Lys Pro Thr Pro
65                  70                  75                  80

Trp Ala Glu Glu Glu Thr Val Ala Ala Ala Gln Leu Ile Thr Met Leu
                85                  90                  95

Trp Ser Leu Ser Val Ser Ser Phe Ala Val Gly Gly Met Thr Ala Ser
            100                 105                 110

Phe Phe Gly Gly Trp Leu Gly Asp Thr Leu Gly Arg Ile Lys Ala Met
        115                 120                 125

Leu Val Ala Asn Ile Leu Ser Leu Val Gly Ala Leu Leu Met Gly Phe
    130                 135                 140

Ser Lys Leu Gly Pro Ser His Ile Leu Ile Ile Ala Gly Arg Ser Ile
145                 150                 155                 160

Ser Gly Leu Tyr Cys Gly Leu Ile Ser Gly Leu Val Pro Met Tyr Ile
                165                 170                 175

Gly Glu Ile Ala Pro Thr Ala Leu Arg Gly Ala Leu Gly Thr Phe His
            180                 185                 190

Gln Leu Ala Ile Val Thr Gly Ile Leu Ile Ser Gln Ile Ile Gly Leu
        195                 200                 205

Glu Phe Ile Leu Gly Asn Tyr Asp Leu Trp His Ile Leu Leu Gly Leu
    210                 215                 220
```

Ser Gly Val Arg Ala Ile Leu Gln Ser Leu Leu Phe Phe Cys Pro
225 230 235 240

Glu Ser Pro Arg Tyr Leu Tyr Ile Lys Leu Asp Glu Glu Val Lys Ala
245 250 255

Lys Gln Ser Leu Lys Arg Leu Arg Gly Tyr Asp Asp Val Thr Lys Asp
260 265 270

Ile Asn Glu Met Arg Lys Glu Arg Glu Glu Ala Ser Ser Glu Gln Lys
275 280 285

Val Ser Ile Ile Gln Leu Phe Thr Asn Ser Ser Tyr Arg Gln Pro Ile
290 295 300

Leu Val Ala Leu Met Leu His Val Ala Gln Gln Phe Ser Gly Ile Asn
305 310 315 320

Gly Ile Phe Tyr Tyr Ser Thr Ser Ile Phe Gln Thr Ala Gly Ile Ser
325 330 335

Lys Pro Val Tyr Ala Thr Ile Gly Val Gly Ala Val Asn Met Val Phe
340 345 350

Thr Ala Val Ser Val Phe Leu Val Glu Lys Ala Gly Arg Arg Ser Leu
355 360 365

Phe Leu Ile Gly Met Ser Gly Met Phe Val Cys Ala Ile Phe Met Ser
370 375 380

Val Gly Leu Val Leu Leu Asn Lys Phe Ser Trp Met Ser Tyr Val Ser
385 390 395 400

Met Ile Ala Ile Phe Leu Phe Val Ser Phe Phe Glu Ile Gly Pro Gly
405 410 415

Pro Ile Pro Trp Phe Met Val Ala Glu Phe Phe Ser Gln Gly Pro Arg
420 425 430

Pro Ala Ala Leu Ala Ile Ala Ala Phe Ser Asn Trp Thr Cys Asn Phe
435 440 445

Ile Val Ala Leu Cys Phe Gln Tyr Ile Ala Asp Phe Cys Gly Pro Tyr
450 455 460

Val Phe Phe Leu Phe Ala Gly Val Leu Leu Ala Phe Thr Leu Phe Thr

465 470 475 480

Phe Phe Lys Val Pro Glu Thr Lys Gly Lys Ser Phe Glu Glu Ile Ala
485 490 495

Ala Glu Phe Gln Lys Lys Ser Gly Ser Ala His Arg Pro Lys Ala Ala
500 505 510

Val Glu Met Lys Phe Leu Gly Ala Thr Glu Thr Val
515 520

<210> 40
<211> 496
<212> PRT
<213> Homo sapiens

<400> 40

Met Gly Thr Gln Lys Val Thr Pro Ala Leu Ile Phe Ala Ile Thr Val
1 5 10 15

Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile Asn
20 25 30

Ala Pro Glu Lys Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr Asp
35 40 45

Lys Gly Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Ser Leu Trp Ser
50 55 60

Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe Ser
65 70 75 80

Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu Ile
85 90 95

Val Asn Leu Leu Ala Val Thr Gly Gly Cys Phe Met Gly Leu Cys Lys
100 105 110

Val Ala Lys Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile Gly
115 120 125

Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly Glu
130 135 140

Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln Leu
145 150 155 160

```
Gly Ile Val Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu Phe
                165                 170                 175

Ile Leu Gly Ser Glu Glu Leu Trp Pro Leu Leu Leu Gly Phe Thr Ile
            180                 185                 190

Leu Pro Ala Ile Leu Gln Ser Ala Ala Leu Pro Phe Cys Pro Glu Ser
        195                 200                 205

Pro Arg Phe Leu Leu Ile Asn Arg Lys Glu Glu Glu Asn Ala Lys Gln
    210                 215                 220

Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile Gln
225                 230                 235                 240

Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val Thr
                245                 250                 255

Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile Ile
            260                 265                 270

Ser Ile Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val
        275                 280                 285

Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Glu Pro
    290                 295                 300

Ile Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Ile Phe Thr Val
305                 310                 315                 320

Val Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Met
                325                 330                 335

Ile Gly Leu Gly Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val Ser
            340                 345                 350

Leu Leu Leu Lys Asp Asn Tyr Asn Gly Met Ser Phe Val Cys Ile Gly
        355                 360                 365

Ala Ile Leu Val Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro Ile
    370                 375                 380

Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala
385                 390                 395                 400
```

Ala Met Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu Val
405 410 415

Gly Leu Leu Phe Pro Ser Ala Ala His Tyr Leu Gly Ala Tyr Val Phe
420 425 430

Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe Phe
435 440 445

Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg Ala
450 455 460

Phe Glu Gly Gln Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly Val
465 470 475 480

Met Glu Met Asn Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn Val
485 490 495

<210> 41
<211> 509
<212> PRT
<213> Homo sapiens

<400> 41

Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
1 5 10 15

Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
20 25 30

Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
35 40 45

Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
50 55 60

Gly Pro Glu Gly Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu
65 70 75 80

Trp Ala Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser
85 90 95

Phe Leu Ile Gly Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met
100 105 110

Leu Val Asn Asn Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu
115 120 125

```
Ala Asn Ala Ala Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu
    130                 135                 140

Ile Gly Ala Tyr Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val
145                 150                 155                 160

Gly Glu Ile Ala Pro Thr His Leu Arg Gly Ala Leu Gly Thr Leu Asn
                165                 170                 175

Gln Leu Ala Ile Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly Leu
            180                 185                 190

Glu Ser Leu Leu Gly Thr Ala Ser Leu Trp Pro Leu Leu Leu Gly Leu
        195                 200                 205

Thr Val Leu Pro Ala Leu Leu Gln Leu Val Leu Leu Pro Phe Cys Pro
    210                 215                 220

Glu Ser Pro Arg Tyr Leu Tyr Ile Ile Gln Asn Leu Glu Gly Pro Ala
225                 230                 235                 240

Arg Lys Ser Leu Lys Arg Leu Thr Gly Trp Ala Asp Val Ser Gly Val
                245                 250                 255

Leu Ala Glu Leu Lys Asp Glu Lys Arg Lys Leu Glu Arg Glu Arg Pro
            260                 265                 270

Leu Ser Leu Leu Gln Leu Leu Gly Ser Arg Thr His Arg Gln Pro Leu
        275                 280                 285

Ile Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn
    290                 295                 300

Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Thr Ala Gly Val Gly
305                 310                 315                 320

Gln Pro Ala Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Val Phe
                325                 330                 335

Thr Leu Val Ser Val Leu Leu Val Glu Arg Ala Gly Arg Arg Thr Leu
            340                 345                 350

His Leu Leu Gly Leu Ala Gly Met Cys Gly Cys Ala Ile Leu Met Thr
        355                 360                 365
```

Val Ala Leu Leu Leu Leu Glu Arg Val Pro Ala Met Ser Tyr Val Ser
370 375 380

Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly
385 390 395 400

Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
405 410 415

Pro Ala Ala Met Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
420 425 430

Ile Ile Gly Met Gly Phe Gln Tyr Val Ala Glu Ala Met Gly Pro Tyr
435 440 445

Val Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr
450 455 460

Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser
465 470 475 480

Ala Ala Phe His Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro
485 490 495

Ser Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu Asn Asp
500 505

<210> 42
<211> 501
<212> PRT
<213> Homo sapiens

<400> 42

Met Glu Gln Gln Asp Gln Ser Met Lys Glu Gly Arg Leu Thr Leu Val
1 5 10 15

Leu Ala Leu Ala Thr Leu Ile Ala Ala Phe Gly Ser Ser Phe Gln Tyr
20 25 30

Gly Tyr Asn Val Ala Ala Val Asn Ser Pro Ala Leu Leu Met Gln Gln
35 40 45

Phe Tyr Asn Glu Thr Tyr Tyr Gly Arg Thr Gly Glu Phe Met Glu Asp
50 55 60

Phe Pro Leu Thr Leu Leu Trp Ser Val Thr Val Ser Met Phe Pro Phe

65 70 75 80

Gly Gly Phe Ile Gly Ser Leu Leu Val Gly Pro Leu Val Asn Lys Phe
85 90 95

Gly Arg Lys Gly Ala Leu Leu Phe Asn Asn Ile Phe Ser Ile Val Pro
100 105 110

Ala Ile Leu Met Gly Cys Ser Arg Val Ala Thr Ser Phe Glu Leu Ile
115 120 125

Ile Ile Ser Arg Leu Leu Val Gly Ile Cys Ala Gly Val Ser Ser Asn
130 135 140

Val Val Pro Met Tyr Leu Gly Glu Leu Ala Pro Lys Asn Leu Arg Gly
145 150 155 160

Ala Leu Gly Val Val Pro Gln Leu Phe Ile Thr Val Gly Ile Leu Val
165 170 175

Ala Gln Ile Phe Gly Leu Arg Asn Leu Leu Ala Asn Val Asp Gly Trp
180 185 190

Pro Ile Leu Leu Gly Leu Thr Gly Val Pro Ala Ala Leu Gln Leu Leu
195 200 205

Leu Leu Pro Phe Phe Pro Glu Ser Pro Arg Tyr Leu Leu Ile Gln Lys
210 215 220

Lys Asp Glu Ala Ala Ala Lys Lys Ala Leu Gln Thr Leu Arg Gly Trp
225 230 235 240

Asp Ser Val Asp Arg Glu Val Ala Glu Ile Arg Gln Glu Asp Glu Ala
245 250 255

Glu Lys Ala Ala Gly Phe Ile Ser Val Leu Lys Leu Phe Arg Met Arg
260 265 270

Ser Leu Arg Trp Gln Leu Leu Ser Ile Ile Val Leu Met Gly Gly Gln
275 280 285

Gln Leu Ser Gly Val Asn Ala Ile Tyr Tyr Tyr Ala Asp Gln Ile Tyr
290 295 300

Leu Ser Ala Gly Val Pro Glu Glu His Val Gln Tyr Val Thr Ala Gly
305 310 315 320

```
Thr Gly Ala Val Asn Val Val Met Thr Phe Cys Ala Val Phe Val Val
                325                 330                 335

Glu Leu Leu Gly Arg Arg Leu Leu Leu Leu Gly Phe Ser Ile Cys
            340                 345                 350

Leu Ile Ala Cys Cys Val Leu Thr Ala Ala Leu Ala Leu Gln Asp Thr
        355                 360                 365

Val Ser Trp Met Pro Tyr Ile Ser Ile Val Cys Val Ile Ser Tyr Val
    370                 375                 380

Ile Gly His Ala Leu Gly Pro Ser Pro Ile Pro Ala Leu Leu Ile Thr
385                 390                 395                 400

Glu Ile Phe Leu Gln Ser Ser Arg Pro Ser Ala Phe Met Val Gly Gly
                405                 410                 415

Ser Val His Trp Leu Ser Asn Phe Thr Val Gly Leu Ile Phe Pro Phe
            420                 425                 430

Ile Gln Glu Gly Leu Gly Pro Tyr Ser Phe Ile Val Phe Ala Val Ile
        435                 440                 445

Cys Leu Leu Thr Thr Ile Tyr Ile Phe Leu Ile Val Pro Glu Thr Lys
    450                 455                 460

Ala Lys Thr Phe Ile Glu Ile Asn Gln Ile Phe Thr Lys Met Asn Lys
465                 470                 475                 480

Val Ser Glu Val Tyr Pro Glu Lys Glu Glu Leu Lys Glu Leu Pro Pro
                485                 490                 495

Val Thr Ser Glu Gln
            500
```

<210> 43
<211> 477
<212> PRT
<213> Homo sapiens

<400> 43

```
Met Thr Pro Glu Asp Pro Glu Glu Thr Gln Pro Leu Leu Gly Pro Pro
1               5                   10                  15
```

```
Gly Gly Ser Ala Pro Arg Gly Arg Arg Val Phe Leu Ala Ala Phe Ala
            20                  25                  30

Ala Ala Leu Gly Pro Leu Ser Phe Gly Phe Ala Leu Gly Tyr Ser Ser
        35                  40                  45

Pro Ala Ile Pro Ser Leu Gln Arg Ala Ala Pro Pro Ala Pro Arg Leu
    50                  55                  60

Asp Asp Ala Ala Ala Ser Trp Phe Gly Ala Val Val Thr Leu Gly Ala
65                  70                  75                  80

Ala Ala Gly Gly Val Leu Gly Gly Trp Leu Val Asp Arg Ala Gly Arg
                85                  90                  95

Lys Leu Ser Leu Leu Leu Cys Ser Val Pro Phe Val Ala Gly Phe Ala
            100                 105                 110

Val Ile Thr Ala Ala Gln Asp Val Trp Met Leu Leu Gly Gly Arg Leu
        115                 120                 125

Leu Thr Gly Leu Ala Cys Gly Val Ala Ser Leu Val Ala Pro Val Tyr
    130                 135                 140

Ile Ser Glu Ile Ala Tyr Pro Ala Val Arg Gly Leu Leu Gly Ser Cys
145                 150                 155                 160

Val Gln Leu Met Val Val Val Gly Ile Leu Leu Ala Tyr Leu Ala Gly
                165                 170                 175

Trp Val Leu Glu Trp Arg Trp Leu Ala Val Leu Gly Cys Val Pro Pro
            180                 185                 190

Ser Leu Met Leu Leu Leu Met Cys Phe Met Pro Glu Thr Pro Arg Phe
        195                 200                 205

Leu Leu Thr Gln His Arg Arg Gln Glu Ala Met Ala Ala Leu Arg Phe
    210                 215                 220

Leu Trp Gly Ser Glu Gln Gly Trp Glu Asp Pro Pro Ile Gly Ala Glu
225                 230                 235                 240

Gln Ser Phe His Leu Ala Leu Leu Arg Gln Pro Gly Ile Tyr Lys Pro
                245                 250                 255

Phe Ile Ile Gly Val Ser Leu Met Ala Phe Gln Gln Leu Ser Gly Val
```

260 265 270

Asn Ala Val Met Phe Tyr Ala Glu Thr Ile Phe Glu Glu Ala Lys Phe
275 280 285

Lys Asp Ser Ser Leu Ala Ser Val Val Val Gly Val Ile Gln Val Leu
290 295 300

Phe Thr Ala Val Ala Ala Leu Ile Met Asp Arg Ala Gly Arg Arg Leu
305 310 315 320

Leu Leu Val Leu Ser Gly Val Val Met Val Phe Ser Thr Ser Ala Phe
325 330 335

Gly Ala Tyr Phe Lys Leu Thr Gln Gly Gly Pro Gly Asn Ser Ser His
340 345 350

Val Ala Ile Ser Ala Pro Val Ser Ala Gln Pro Val Asp Ala Ser Val
355 360 365

Gly Leu Ala Trp Leu Ala Val Gly Ser Met Cys Leu Phe Ile Ala Gly
370 375 380

Phe Ala Val Gly Trp Gly Pro Ile Pro Trp Leu Leu Met Ser Glu Ile
385 390 395 400

Phe Pro Leu His Val Lys Gly Val Ala Thr Gly Ile Cys Val Leu Thr
405 410 415

Asn Trp Leu Met Ala Phe Leu Val Thr Lys Glu Phe Ser Ser Leu Met
420 425 430

Glu Val Leu Arg Pro Tyr Gly Ala Phe Trp Leu Ala Ser Ala Phe Cys
435 440 445

Ile Phe Ser Val Leu Phe Thr Phe Ser Cys Val Pro Glu Thr Lys Gly
450 455 460

Lys Thr Leu Glu Gln Ile Thr Ala His Phe Glu Gly Arg
465 470 475